

Figure 1B

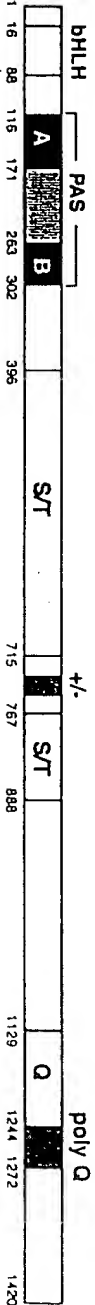


FIGURE 5A: MOUSE AIB1 (pCIP) INTRON/EXON BOUNDARIES

Exon	cDNA bp	cDNA bp	3'intron	Exon sequence		5'intron
				splice site	(5' to 3')	
1		11			GCGGCGAACG	
2	12			GATCAAAAGAATTTGCTGAA		
2		90			CCTTCCTGAACAGCTGTACG	
3	91			TGTCACCTCTTCTCCGCAG		
3		195			TGTGATGCCCCAGGACAGGG	
4	196			GGCTTTTCTCCGCCCTCCAG		
4		368			ACGGCAAATAAAGAACAAG	GTAAACACAGAGTCAGAAAA
5	369			GCCTTCCTCTGTGCTTCAG		
5		469			TAGGACCGCTTTTACTACAG	ATTTTCTTACAAACGAGGCT
6	470			ATTAACACATTCACACTGAG		
6		644			ACACTTACCAAAATCCACAG	GTGGGCTCTTCTTTGTGTTT
7	645			TTTAAATTTGTTTTTCAAG		
7		830			TATGCTGGAAGAAGGAGAAG	GTGAGAGCGGGTCCACTGT
8	831			CTGGTGACCTTTCGTTGTAG		
8		923			TACCAGACATGACCTTTCCG	GTAAAGACCAGTCTTCACTGG
9	924			TCGTGTTTTATCTTTAATAG		
9		1064			GAAAGGTTGTCAATATAGAT	
10	1065			GTGTGCTTCCCCCTCCGTAG		GTGAGGAGGCGTTTGGGGT
10		1212			TCGACCCACTTTCTTCAGAG	GTGATGACACTAAAGCACCC
11	1213			TTGCGTGTGTTGTTTGACG		
11		1589			CCAGTTCCTCCTGCTGCAG	GTATCCACAGCTGCGTTTTC
12	1590			CGACCTTTCTCCATATGCAG		
12		2458			AGACCGAGACGAACGAGAG	GAGGTAAGGTACTCTCTGTT
13	2459			TTTAAAGGTTCAATTTTCAG		
13		2588			TGCAGGACCGAGTTCTCTGG	GTAAAGAAAAACAGAGTTTT
14	2589			AGCTTCTGTGTTTCAACAG		
14		2783			GAATTACGGGTGCCAACATGG	GTAGGTCACTGTCTAAGTGTG

FIGURE 5B: MOUSE AIB1 (pCIP) INTRON/EXON BOUNDARIES

Exon	cDNA bp	cDNA bp	3'intron	Exon sequence		5'intron
				splice site	(5' to 3')	
15	2784		TGAGCCCTCCCTAATTTAG	GCCCAACAGAAATGTTCT		
15		3095			GCAGCAGATGCTTCAATGA	GTAGCTGTCCCTTCAATA
16	3096		ATTTGATTTGCTCCCCAG	GAACTG GTGAGATTCCCATG		
16		3222			CCTCAGGGGTCTCAAAATAG	GTAGGTTTTATTTGGGAT
17	3223		TGACTCAGCTCTCTCTAG	GCC TCTTCTTAGAACTCTC		
17		3394			TTCCTGAGCTCGTGAATCAG	GTGAGTTGCAATCTGTGAG
18	3395		CTTTGTGTTGATGTTTAAAG	GGACAAGCTTTGGAGTCCAA		
18		3688			AGAGGCTACAGGGCCAGCAG	GTAAGACCGGGCTGTCAGGG
19	3689		ACTAACCCAACTCTGTT CAG	TTTTTAAATCAGAGCCGGCA		
19		3772			TGAGGCCCATGATGCCCCAG	GTACGTTCCCTGCAGAGAAG
20	3773		TGTCCTTGGCTACCAGCAG	GCTTTC TTTAATGCCCAAAT		
20		3989			TCCATATCCAGCAAAATTACG	GTAAACCTGTCAGATTGTGC
21	3990		TTTCTGTTCA TTTCTTTAAG	GAA TGGACAACCA CCAGAGAG		
21		4164			GGGAACCTGGCCAAGAA TGG	GTAAAGATGGGACTTACTTT
22	4165		CTGTTACCC TTTCTTTG CAG	CTCCTTCCCCCAGCAGCAGT		
22		4306			TGCCCATGGGCCCGATCAG	GTACGGGCATCTATTCTTAC
23	4307		CTGTGTTCTCTGTTAACAG	AAATACTGCTGACATCTCCC		
23		4622				

FIGURE 6A: HUMAN AIB1 INTRON/EXON BOUNDARIES

cDNA bp		cDNA bp		3'intron		Exon sequence (5' to 3')		5'intron	
Exon	5'exon	3'exon	splice site				splice site		
1		102				GAGGAAAATGGCGGGGAG	GTGAGTGGAGATAAAGGAGG		
2	103		CCTCTTCTTTTGTCTCAG	GATCAAAATACTTGCTGGAT		TCCTTTGACTGGTTAGCCAG	GTAATTCAGCTTtagTTGA		
2		181				TGTGATACTCCAGGACAAGG	GTAGGTGACTTAATTCTCTGG		
3	182		TTCTCATTATTCCTCTTAG	TTGCTGATGTAATTCaAGA		ACGTCAAATAAAAGAGCAAG	GTAAT7AAAAACACTCATGTC		
3		283				TAGGACCGCTTTTACTTCAG	GCAAGTA7AAGATTTTAAc		
4	284		TTCTACGCCCTTTCCCTTAG	TCTTACCTGCAGTGGTGAAA		GAA7TTACCAAAATCTACAG	GTAGGCTTTTAA7GTGTA7T		
4		456				TATGATGGAGGAAGGGGAAG	GTAA7AGAGCTATTATATGTTT		
5	457		ACCACCTTCTGTCTTTTCAG	GAAAAACTATTTCCaATGAT		TACCAGACATGATCTTTTCAG	GTAAAAATCTTTT7TGTCC		
5		557				GAAACGTCACTATCAAGAAG	GTAAAGAA7TTTGGGTTGA		
6	558		ATTAACATATCCTA7TTTAG	GCATTGGATG7TTTCTA7T		TCAGTTTTCCTCTGTTGCAG	G7ATTTGTGTTGACATTTCC		
6		732				AGACAGAGACAAGTGAAGAG	G7AATTTGTTTCTGTATAT		
7	733		TTTCAATTTGTTTCCAAAG	TTAA7GAGTTTCTCGACA		TCAAGAACTAAT7TCTCTGG	G7AAGATGAAGTAAG7TTT		
7		921							
8	922		GGGTGAATTTTATTTAGTAG	ATT7GCAATCTTG7ATGATC					
8		1023							
9	1024		TTCCTTTT7TTGTTAATAG	GAAAG7TGTCAATATAGAT					
9		1164							
10	1165		TGGGATATTTTCCCAACAG	CTATCTTAATG7CCATGCA					
10		1312							
11	1313		GTTTGATGTTTGT7TTGCAG	AGAACAGAA7TGATATAGAC					
11		1704							
12	1705		AAATTTT7TTTCAAAATTCAG	G7GTGCAC7CTCCCATGGCA					
12		2576							
13	2577		TTT7AAAC7TTATTTTCAG	GGATCTG7GAGACTTGAT7AA					
13		2712							

FIGURE 6B: HUMAN AIB1 INTRON/EXON BOUNDARIES

Exon	cDNA bp	cDNA bp	3'intron		Exon sequence		5'intron
			splice site		(5' to 3')		
14	2713	2907	TTGTATTGTTTTCACAG	GTTTGAAAAGTTCACAGTCT	AAATTATGGCTCAAGTATGG	GTATGTTATTTCTAATTAGT	
14			AGTATGGCTACCTGTTTTAG	GTGGGCCAAACCGAAATGTG	TCTCATGGCACTCAAATAG	GTGGGTGTTATTTGTGAC	
15	2908	3280	GATTGCAAGTCTTTTTCTAG	GCCTCTTCTTAGGAATTTCCC	TTCTGAACTTGTCAATCAG	GTAGTTGCATTAACATGGA	
16	3281	3452	TTTATGTGTTGTTTAAAG	GGACAGGCATTAGAGCCCAA	AGAGGCTGCAGGGCCAGCAG	GTAAACCAGTCATGTGTTCTT	
17	3453	3746	ACCAACTTGTCTCACCCTCAG	TTTTTGAATCAGAGCCGACA	GGCCTATGATGCAGCCCCAG	GTGAGCTCCAGGTGAGGAT	
18	3747	3839	CACTCTTCTTGGGTAATTAG	CAGGGTTTCTTAATGCTCA	TCCATATCAACCAAAATTATG	GTAAATCTGACCAATGAAAT	
19	3840	4134	TTCTGTTTATTTTTGTAAAG	GAATGGGACAAACAACAGAT	GGAAATTTGGCCAGGAACAG	GTAAAGAACAGTGACTTATA	
20	4135	4309	TACCATTGTTTACTTACAG	CTCCTTTTCCACAGCAGCAGT	TGCCTATGGGTCCTGATCAG	GTATGGGATCGATTCCTTAC	
21	4310	4450	TTTTTCCTGTTGCTGACAG	AAATACTGCTGACATCTCTG			
22	4451						
(18)							